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=> s ((yeast# or saccharomyces or cerevisiae)(10a)genom?)/bi,ab 199350 YEAST#/BI
168818 YEAST#/AB 83517 SACCHAROMYCES/BI
48233 SACCHAROMYCES/AB 77161 CEREVISIAE/BI
53322 CEREVISIAE/AB 212948 GENOM?/BI
193343 GENOM?/AB
L1 5174 ((YEAST# OR SACCHAROMYCES OR CEREVISIAE)(10A)GENOM?)/BI,AB

=> s (sequence (10a) compar?)/bi,ab 676935 SEQUENCE/BI
498734 SEQUENCE/AB 2922514 COMPAR?/BI
2761413 COMPAR?/AB
L2 30550 (SEQUENCE (10A) COMPAR?)/BI,AB

=> s (array? or microarray?)/bi,ab 142155 ARRAY?/BI
132301 ARRAY?/AB 37421 MICROARRAY?/BI
20644 MICROARRAY?/AB
L3 171023 (ARRAY? OR MICROARRAY?)/BI,AB

=> s l2 or l3
L4 201026 L2 OR L3

=> s l1 and l4
L5 679 L1 AND L4

=> s l5 not 2006/py 135818 2006/PY
L6 672 L5 NOT 2006/PY

=> s l6 not 2004/py 1286255 2004/PY
L7 553 L6 NOT 2004/PY

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L2 30550 S (SEQUENCE (10A) COMPAR?)/BI,AB
L3 171023 S (ARRAY? OR MICROARRAY?)/BI,AB
L4 201026 S L2 OR L3
L5 679 S L1 AND L4
L6 672 S L5 NOT 2006/PY
L7 553 S L6 NOT 2004/PY

=> s ((nucleic(w)acid#) or gene# or dna#)/bi,ab 179165 NUCLEIC/BI 75775 NUCLEIC/AB 4590923 ACID#/BI 3090247 ACID#/AB 178162 NUCLEIC(W)ACID# 1074758 GENE#/BI 820232 GENE#/AB 761845 DNA#/BI 593947 DNA#/AB
L8 1529420 ((NUCLEIC(W)ACID#) OR GENE# OR DNA#)/BI,AB

=> l5 and l8
L5 IS NOT A RECOGNIZED COMMAND
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=> s l5 and l8
L9 642 L5 AND L8

=> s (industrial(w)yeast#)/bi,ab 252207 INDUSTRIAL/BI 167823 INDUSTRIAL/AB 199350 YEAST#/BI 168818 YEAST#/AB
L10 288 (INDUSTRIAL(W)YEAST#)/BI,AB

=> s l9 and l10
L11 3 L9 AND L10

=> s industrial/bi,ab 252207 INDUSTRIAL/BI 167823 INDUSTRIAL/AB
L12 252207 INDUSTRIAL/BI,AB

=> s l9 and l12
L13 10 L9 AND L12

=> d his
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FILE 'CAPLUS' ENTERED AT 20:08:22 ON 17 FEB 2006
L1 5174 S ((YEAST# OR SACCHAROMYCES OR CEREVISIAE)(10A)GENOM?)/BI,AB
L2 30550 S (SEQUENCE (10A) COMPAR?)/BI,AB
L3 171023 S (ARRAY? OR MICROARRAY?)/BI,AB
L4 201026 S L2 OR L3
L5 679 S L1 AND L4
L6 672 S L5 NOT 2006/PY
L7 553 S L6 NOT 2004/PY
L8 1529420 S ((NUCLEIC(W)ACID#) OR GENE# OR DNA#)/BI,AB
L9 642 S L5 AND L8
L10 288 S (INDUSTRIAL(W)YEAST#)/BI,AB
L11 3 S L9 AND L10
L12 252207 S INDUSTRIAL/BI,AB
L13 10 S L9 AND L12

=> d l13 1-10 bib ab

L13 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:756902 CAPLUS
DN 141:255505

TI ***DNA*** ***microarrays*** and methods for screening a brewing ***yeast*** ***genome*** and identifying ***genes*** to improve alcoholic beverages
IN Nakao, Yoshihiro; Nakamura, Norihisa; Kodama, Yukiko; Fujimura, Tomoko; Ashikari, Toshihiko
PA Suntory Limited, Japan
SO PCT Int. Appl., 133 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI WO 2004079008 A1 20040916 WO 2004-JP2695 20040303 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG CA 2518046 AA 20040916 CA 2004-2518046 20040303 JP 2004283169 A2 20041014 JP 2004-59843 20040303 EP 1599605 A1 20051130 EP 2004-716716 20040303 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK US 2004265862 A1 20041230 US 2004-791791 20040304
PRAI JP 2003-57677 A 20030304 WO 2004-JP2695 W 20040303
AB The invention provides a method for the selection of ***genes*** participating in a desired brewing character and the method involves prepg. a database of the whole ***genome*** sequence and data of ***industrial*** ***yeast*** , particularly of a brewing ***yeast*** used for alc. beverages such as beer. ***Genes*** participating in a brewing character that the brewing yeast specifically possesses are selected from the database and functional anal. of the ***genes*** are carried out by disruption or overexpression. The means for achieving the above objects is a screening method for ***genes*** participating in increase in productivity and/or improvement in flavor in the prodn. of an alc. or an alc. beverage, characterized in that, (A) the whole ***genome*** ***sequence*** of ***industrial*** ***yeast*** is analyzed, (B) the ***genome*** ***sequence*** is ***compared*** with the whole ***genome*** ***sequence*** of S. ***cerevisiae*** , (C) ***gene*** of the ***industrial*** ***yeast*** encoding an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the ***gene*** of S. cerevisiae is selected and (D) functional anal. of the ***gene*** is carried out, whereby the character which is given to the yeast by the ***gene*** is identified. Brewing ***yeast*** is a polyploid, with part of its ***genome*** thought to be derived from ***Saccharomyces*** ***cerevisiae*** . The invention claims use of a ***DNA*** ***array*** that is based on the database of the whole ***genome*** sequences of an ***industrial*** ***yeast*** or of a brewing ***yeast*** . The invention further claims methods for breeding of yeast, such as genetic hybridization, to achieve the brewing character which the identified ***gene*** participates in. A recombinant or hybrid brewing yeast strain can be used for the prodn. of an alc. or an alc. beverage with improved productivity and quality. Still another object of the invention is to provide a ***gene*** which is specific to the

brewing yeast and a polypeptide encoded by the ***gene*** . The invention provides polynucleotide and polypeptide sequences for Saccharomyces ***genes*** SSU1 and MET14 involved in sulfite prodn.
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:622291 CAPLUS
DN 141:255013
TI ***Yeast*** ***genome*** sequencing: The power of comparative ***genomics***
AU Piskur, Jure; Langkjaer, Rikke B.
CS BioCentrum-DTU, Technical University of Denmark, Kgl. Lyngby, DK-2800, Den.
SO Molecular Microbiology (2004), 53(2), 381-389 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Publishing Ltd.
DT Journal; General Review
LA English
AB A review. For decades, unicellular yeasts have been general models to help understand the eukaryotic cell and also our own biol. Recently, over a dozen ***yeast*** ***genomes*** have been sequenced, providing the basis to resolve several complex biol. questions. Anal. of the novel sequence data has shown that the min. no. of ***genes*** from each species that need to be compared to produce a reliable phylogeny is about 20. Yeast has also become an attractive model to study speciation in eukaryotes, esp. to understand mol. mechanisms behind the establishment of reproductive isolation. Comparison of closely related species helps in ***gene*** annotation and to answer how many ***genes*** there really are within the genomes. Anal. of non-coding regions among closely related species has provided an example of how to det. novel ***gene*** regulatory sequences, which were previously difficult to analyze because they are short and degenerate and occupy different positions. Comparative ***genomics*** helps to understand the origin of ***yeasts*** and points out crucial mol. events in ***yeast*** evolutionary history, such as whole- ***genome*** duplication and horizontal ***gene*** transfer(s). In addn., the accumulating sequence data provide the background to use more yeast species in model studies, to combat pathogens and for efficient manipulation of ***industrial*** strains.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:425674 CAPLUS
DN 141:67886
TI Postgenome study of fission yeast. The smallest number of ***genes*** in a eukaryote
AU Tohda, Hideki; Hama, Yuko Giga; Takegawa, Kaoru
CS Aspex Div., Asahi Glass Co., Ltd., Yokohama, 221-8755, Japan
SO Baiosaiensu to Indasutori (2004), 62(5), 316-319 CODEN: BIDSE6; ISSN: 0914-8981
PB Baioindasutori Kyokai
DT Journal; General Review
LA Japanese
AB A review on the genome structure of Schizosaccharomyces pombe, prepn. of ***DNA*** ***microarray*** of S. pombe, functional anal. of alc. dehydrogenase ***genes*** by ***DNA*** ***microarray*** , ***genes*** whose expression levels were increased or decreased during recombinant protein prodn., other post- ***genomic*** studies on S. pombe, and ***industrial*** application of fission ***yeast*** .

L13 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:651862 CAPLUS
DN 139:304311
TI ***Yeast*** ***genome*** -wide expression analysis identifies a strong ergosterol and oxidative stress response during the initial stages of an ***industrial*** lager fermentation
AU Higgins, Vincent J.; Beckhouse, Anthony G.; Oliver, Anthony D.; Rogers, Peter J.; Dawes, Ian W.
CS Clive and Vera Ramaciotti Centre for Gene Function Analysis and School of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, 2052, Australia
SO Applied and Environmental Microbiology (2003), 69(8), 4777-4787 CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB ***Genome*** -wide expression anal. of an ***industrial*** strain of ***Saccharomyces*** ***cerevisiae*** during the initial stages of an ***industrial*** lager fermn. identified a strong response from ***genes*** involved in the biosynthesis of ergosterol and oxidative stress protection. The induction of the ERG ***genes*** was confirmed by Northern anal. and was found to be complemented by a rapid accumulation of ergosterol over the initial 6-h fermn. period. From a test of the metabolic activity of deletion mutants in the ergosterol biosynthesis pathway, it was found that ergosterol is an important factor in restoring the fermentative capacity of the cell after storage. Addnl., similar ERG10 and TRR1 ***gene*** expression patterns over the initial 24-h fermn. period highlighted a possible interaction between ergosterol biosynthesis and the oxidative stress response. Further anal. showed that erg mutants producing altered sterols were highly sensitive to oxidative stress-generating compds. Here we show that genome-wide expression anal. can be used in the com. environment and was successful in identifying environmental conditions that are important in ***industrial*** yeast fermn.
RE.CNT 70 THERE ARE 70 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:363722 CAPLUS
DN 139:226883
TI ***Genome*** -wide expression analyses: metabolic adaptation of ***Saccharomyces*** ***cerevisiae*** to high sugar stress
AU Erasmus, Daniel J.; Van Der Merwe, George K.; Van Vuuren, Hennie J. J.
CS Faculty of Agricultural Sciences, Wine Research Centre, The University of British Columbia, Vancouver, BC, V6T 1Z4, Can.
SO FEMS Yeast Research (2003), 3(4), 375-399 CODEN: FYREAG; ISSN: 1567-1356
PB Elsevier Science B.V.
DT Journal; General Review
LA English
AB A review. The transcriptional response of lab. strains of S. cerevisiae to salt or sorbitol stress has been well studied. These studies have yielded valuable data on how the yeast adapts to these stress conditions. However, S. cerevisiae is a saccharophilic fungus and in its natural environment this yeast encounters high

concns. of sugars. For the prodn. of dessert wines, the sugar concn. may be as high as 50%. The metabolic pathways in S. cerevisiae under these fermn. conditions have not been studied and the transcriptional response of this yeast to sugar stress has not been investigated. High-d. ***DNA*** ***microarrays*** showed that the transcription of 589 ***genes*** in an ***industrial*** strain of S. cerevisiae were affected >2-fold in grape juice contg. 40% sugars (equimolar amts. of glucose and fructose). High sugar stress up-regulated the glycolytic and pentose phosphate pathway ***genes*** . The PDC6 ***gene*** , previously thought to encode a minor isoenzyme of pyruvate decarboxylase, was highly induced under these conditions. ***Gene*** expression profiles indicate that the oxidative and non-oxidative branches of the pentose phosphate pathway were up-regulated and might be used to shunt more glucose 6-phosphate and fructose 6-phosphate, resp., from the glycolytic pathway into the pentose phosphate pathway. Structural ***genes*** involved in the formation of acetic acid from acetaldehyde, and succinic acid from glutamate, were also up-regulated. ***Genes*** involved in de novo biosynthesis of purines, pyrimidines, histidine and lysine were down-regulated by sugar stress.
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:599679 CAPLUS
DN 136:182588
TI Functional ***genomics*** applied to enological ***yeasts***
AU Blondin, B.; Luyten, Kattie; Riou, Christine
CS Laboratoire de Microbiologie et Technologie des Fermentations INRA-AgroMontpellier, Institut des Produits de la Vigne, Montpellier, 34060, Fr.
SO Bulletin de l'O.I.V. (2001), 74(841-842), 201-208 CODEN: BLOVAJ; ISSN: 0029-7127
PB Office International de la Vigne et du Vin
DT Journal; General Review
LA French
AB A review. The availability of the ***yeast*** ***genome*** sequence together with the development of new tools of functional ***genomic*** open a new era in the study of ***industrial*** enol. ***yeasts*** . The 6200 putative ***genes*** of Saccharomyces cerevisiae are now known and, in our context, an important challenge will be to ascribe a role to these ***genes*** with respect to the technol. properties of the strains. The knowledge of the ***genes*** and the availability of powerful genetic tools in yeast allow systematic anal. to specify the involvement of any ***gene*** in cell functions important during alc. fermn. As an example, we have assessed the role of individual hexose transport HXT ***genes*** during alc. fermn. Using an approach based on ***gene*** disruption and anal. of the impact on the fermn. properties of the yeast, we show that only two hexose carriers, among a family of 18 ***genes*** , play an important, but different, role during alc. fermn. These data should help to define new strategies to improve sugar utilization by yeast. Tools of functional genomic such as ***DNA*** ***arrays*** which allow the simultaneous anal. of the expression level of all the 6200 yeast ***genes*** represent a technol. breakthrough in the study of ***industrial*** yeasts. The knowledge of ***gene*** expression profiles will be a key element in the understanding of the mol. mechanism involved in yeast properties. We have used ***DNA*** mini-***arrays*** anal. to examine the expression of the ***genome*** of an ***industrial*** ***yeast*** during alc. fermn. These approaches allowed as to identify a large set of ***genes*** which are highly expressed during alc. fermn. and to monitor their expression during a fermn. cycle. The interest of global transcriptome anal. in deciphering the mol. bases of strain properties is discussed.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:361344 CAPLUS
DN 136:80617
TI Whole ***genome*** analysis of a wine ***yeast*** strain
AU Hauser, Nicole C.; Fellenberg, Kurt; Gil, Rosario; Bastuck, Sonja; Hoheisel, Jorg D.; Perez-Ortin, Jose E.
CS Functional Genome Analysis, Deutsches Krebsforschungszentrum, Heidelberg, D-69120, Germany
SO Comparative and Functional Genomics (2001), 2(2), 69-79 CODEN: CFGOAT; ISSN: 1531-6912
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Saccharomyces cerevisiae strains frequently exhibit rather specific phenotypic features needed for adaptation to a special environment. Wine yeast strains are able to ferment musts, for example, while other ***industrial*** or lab. strains fail to do so. The genetic differences that characterize wine yeast strains are poorly understood, however. As a first search of genetic differences between wine and lab. strains, we performed ***DNA*** - ***array*** analyses on the typical wine yeast strain T73 and the std. lab. background in S288c. Our anal. shows that even under normal conditions, logarithmic growth in YPD medium, the two strains have expression patterns that differ significantly in more than 40 ***genes*** . Subsequent studies indicated that these differences correlate with small changes in promoter regions or variations in ***gene*** copy no. Blotting copy nos. vs. transcript levels produced patterns, which were specific for the individual strains and could be used for a characterization of unknown samples.
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:197593 CAPLUS
TI ***Genome*** -wide monitoring of transcriptional response of the ***yeast*** , S. ***cerevisiae*** , to a bioactive contaminant
AU Xu, Deming; Brooker, Deborah; McNeil, Bryan; McCarry, Brian; Friesen, James D.; Yager, Thomas
CS C.H. Best Microarray Center, BBDMR, University of Toronto, Toronto, ON, M5G 1L6, Can.
SO Abstracts of Papers, 221st ACS National Meeting, San Diego, CA, United States, April 1-5, 2001 (2001) BTEC-018 CODEN: 69FZD4
PB American Chemical Society
DT Journal; Meeting Abstract
LA English
AB Coal tar is a complex mixt. of PAH compds. produced from ***industrial*** processes. To assess its bioactivities, we choose ***yeast*** , S. ***cerevisiae*** , and used whole ***genome*** ***DNA*** chips and ***microarray*** technique to examine transcriptional response to coal tar. Although yeast cells are resistant to coal tar, such a treatment

causes significant physiol. changes that affect the initial growth. We purified total RNA from treated and control samples. Poly(A)+ mRNAs were converted to cDNA in the presence of fluorescent nucleotides. ***DNA*** chips were then hybridized with mixt. of differentially labeled cDNAs. The intensities of fluorescent signals bound to different ***genes*** represent the relative abundance of mRNAs and any changes reflect the changes in response to coal tar in the medium. Our anal. of six ***microarray*** data has revealed consistent changes of a fraction of the ***yeast*** ***genome*** in response to coal tar. We are currently focusing on interpretation of the results.

L13 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:24051 CAPLUS
DN 134:247823
TI Genomic Exploration of the Hemiascomycetous Yeasts: 16. Candida tropicalis
AU Blandin, G.; Ozier-Kalogeropoulos, O.; Wincker, P.; Artiguenave, F.; Dujon, B.
CS Unite de Genetique Moleculaire des Levures, Departement des Biotechnologies, URA 2171 CNRS, UFR 927 Univ. P. and M. Curie, Institut Pasteur, Paris, F-75724, Fr.
SO FEBS Letters (2000), 487(1), 91-94 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB The genome of the diploid hemiascomycetous yeast Candida tropicalis, an opportunistic human pathogen and an important organism for industrial applications, was explored by the anal. of 2541 Random Sequenced Tags (RSTs) covering about 20% of its genome. Comparison of these sequences with Saccharomyces cerevisiae and other species permitted the identification and the anal. of a total of >1000 novel genetic elements of C. tropicalis. Moreover, the present study confirms that in C. tropicalis, the rare CUG codon is read as a serine and not a leucine. The sequences have been deposited at EMBL with the accession nos. AL438875-AL441602.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1991:507197 CAPLUS
DN 115:107197
TI Evidence for cis- and trans-acting element coevolution of the 2-.mu.m circle ***genome*** in ***Saccharomyces*** ***cerevisiae***
AU Xiao, Wei; Pelcher, Lawrence E.; Rank, Gerald H.
CS Dep. Biol., Univ. Saskatchewan, Saskatoon, SK, S7N 0W0, Can.
SO Journal of Molecular Evolution (1991), 32(2), 145-52 CODEN: JMEVAU; ISSN: 0022-2844
DT Journal
LA English
AB The authors ***compared*** the ***DNA*** ***sequence*** of the yeast 2-.mu.m plasmid cis-acting STB and trans-acting REP1 partition loci of lab. haploid and ***industrial*** amphiploid strains. Several ***industrial*** strains had a unique STB sequence (type 1) sharing only 70% homol. with lab. STB (type 2). Type 1 plasmids had a REP1 protein with 6-10% amino acid substitutions when compared to REP1 of type 2 plasmids. All 2-.mu.m variants that shared a similar STB consensus sequence exhibited a high degree of REP1 nucleotide and amino acid sequence conservation. These observations suggest mol. coevolution of trans-acting elements with cognate target ***DNA*** structure. Based on ***DNA*** sequencing and Southern hybridization analyses, the authors classified 2-.mu.m variants into two main evolutionary lineages that differ at STB as well as REP1 loci. The role of mol. coevolution in yeast intra- and interspecies plasmid evolution was discussed.

=> s alcohol?/bi,ab 397419 ALCOHOL?/BI 29786 ALCOHOL?/AB
L14 397419 ALCOHOL?/BI,AB

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L15 6 L9 AND L14

=> d his
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L1 5174 S ((YEAST# OR SACCHAROMYCES OR CEREVISIAE)(10A)GENOM?)/BI,AB
L2 30550 S (SEQUENCE (10A) COMPAR?)/BI,AB
L3 171023 S (ARRAY? OR MICROARRAY?)/BI,AB
L4 201026 S L2 OR L3
L5 679 S L1 AND L4
L6 672 S L5 NOT 2006/PY
L7 553 S L6 NOT 2004/PY
L8 1529420 S ((NUCLEIC(W)ACID#) OR GENE# OR DNA#)/BI,AB
L9 642 S L5 AND L8
L10 288 S (INDUSTRIAL(W)YEAST#)/BI,AB
L11 3 S L9 AND L10
L12 252207 S INDUSTRIAL/BI,AB
L13 10 S L9 AND L12
L14 397419 S ALCOHOL?/BI,AB
L15 6 S L9 AND L14

=> s l15 not l13
L16 5 L15 NOT L13

=> d l16 1-5 bib ab

L16 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2005:409710 CAPLUS
DN 142:458158
TI Markers for glioma classification identified by comparative genomic hybridization ***gene*** expression analysis
IN Harris, Cole; Davis, Lisa
PA Exagen Diagnostics, USA
SO PCT Int. Appl., 43 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2005042786 A2 20050512 WO 2004-US38393 20041103 WO 2005042786 A3 20050901 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB,

GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2005181389 A1 20050818 US 2004-981277 20041103
PRAI US 2003-516817P P 20031103
AB The present invention provides novel compns. and their use in classifying gliomas. In a preferred embodiment, the methods are used to discriminate between oligodendroglioma and glioblastoma. The present invention provides novel compns. and methods for their use in classifying gliomas, particularly to distinguish between glioma types such as oligodendrogliomas and glioblastomas. Malignant gliomas are the most common primary brain tumor, and are classified histol., with pathol. diagnosis affecting prognostic estn. and therapeutic decision-making more than any other variable. The inventors of the present invention have identified compns. to permit improved glioma classification over that possible using prior art diagnostic and predictive compns. and methods. Based on the above anal., they have identified the following ***genes*** showing statistical significance ($p<.05$) as glioma markers (ie: they tend to be present in decreased copy no. in oligodendrogliomas relative to glioblastomas, and they tend to be expressed at a lower level in oligodendrogliomas relative to glioblastomas), based on the combined anal. of CGH and ***gene*** expression data:.

L16 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:610997 CAPLUS
DN 141:328243
TI New method for the assessment of biological effect by surfactants using yeast ***DNA*** ***microarray***
AU Kurita, Sakiko; Sirisattha, Sophon; Kitagawa, Emiko; Momose, Yuko; Akama, Kuniko; Ishigami, Yutaka; Iwahashi, Hitoshi
CS National Institute of Advanced Industrial Science and Technology, Tsukuba, 305-8566, Japan
SO Journal of Oleo Science (2004), 53(8), 387-398 CODEN: JOSOAP; ISSN: 1345-8957
PB Japan Oil Chemists' Society
DT Journal
LA English
AB Spiculisporic acid (a biosurfactant produced by Penicillium spiculisporum) is used in the prepn. of detergents, gelation agents, coloring agents for concrete, vesicle forming agents, etc. The effects of biosurfactant and synthetic surfactants (SDS and LAS) were assessed for the first time in this study at the ***genomic*** level by ***yeast*** ***DNA*** ***microarray*** bioassay. Hierarchical clustering showed spiculisporic acid to be close to LAS and SDS. The effects of spiculisporic acid on yeast cells would thus appear basically the same as those of LAS and SDS. ***Gene*** induction by spiculisporic acid was particularly remarkable in functional categories of "metab.", while "cell rescue defense and virulence" and "energy" categories differed from those with SDS and LAS. Thus, spiculisporic acid and SDS might be metabolized via beta-oxidn. in two different organelles, mitochondria and peroxisome, resp. This would explain the low oxidative stress with spiculisporic acid, vs. the high oxidative stress with SDS.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:10576 CAPLUS
DN 140:196043
TI ***Genome*** -wide monitoring of wine ***yeast*** ***gene*** expression during ***alcoholic*** fermentation
AU Rossignol, Tristan; Dulau, Laurent; Julien, Anne; Blondin, Bruno
CS UMR Sciences Pour l'Oenologie INRA-ENSAM, Microbiologie et Technologie des Fermentations, Montpellier, 34060, Fr.
SO Yeast (2003), 20(16), 1369-1385 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The transcriptome of a wine yeast was monitored throughout an alc. fermn. under conditions mimicking an enol. environment. Major changes in ***gene*** expression occurred during fermn., affecting more than 2000 ***genes*** , as the yeast adapted to changing nutritional, environmental and physiol. conditions. The ***genes*** of many pathways are regulated in a highly coordinated manner, and ***genes*** involved in the key metabolic pathways of fermn. are strongly expressed. We showed that, during fermn. of a synthetic medium mimicking a natural must in which growth arrest was caused by nitrogen exhaustion, entry into the stationary phase triggered major transcriptional reprogramming. Many TOR target ***genes*** involved in nitrogen utilization or other functions are induced at this stage, suggesting that this signalling pathway plays a crit. role in changes in ***gene*** expression in response to nitrogen depletion. Entry into stationary phase is a key physiol. event and is followed by a general stress response. The superimposition of multiple stresses, including starvation and ethanol stress, gives rise to a unique stress response, involving hundreds of ***genes*** encoding proteins involved in various cellular processes, many of unknown function.
RE.CNT 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:268122 CAPLUS
DN 138:400489
TI Transcription profile of brewery yeast under fermentation conditions
AU James, T. C.; Campbell, S.; Donnelly, D.; Bond, U.
CS Moyne Institute for Preventive Medicine, Microbiology Department, Trinity College, University of Dublin, Dublin 2, Ire.
SO Journal of Applied Microbiology (2003), 94(3), 432-448 CODEN: JAMIFK; ISSN: 1364-5072
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB Aims: Yeast strains, used in the brewing industry, experience distinctive physiol. conditions. During a brewing fermn., yeast are exposed to anaerobic conditions, high pressure, high sp. gr. and low temps. The purpose of this study was to examine the global ***gene*** expression profile of yeast subjected to brewing stress. Methods and Results: We have carried out a ***microarray*** anal. of a typical brewer's yeast during the course of an 8-day fermn. in 15.degree.P wort. We used the probes derived from ***Saccharomyces*** ***cerevisiae*** ***genomic*** ***DNA*** on the chip and RNA isolated from three stages of brewing. This anal. shows a high level of expression of ***genes*** involved in fatty acid and ergosterol biosynthesis early in fermn. Furthermore, ***genes*** involved in respiration and mitochondrial protein synthesis also show higher levels of expression. Conclusions: Surprisingly, we obsd. a complete repression of many stress response ***genes*** and ***genes*** involved in protein synthesis throughout the 8-day period compared with that at the start of fermn. Significance and Impact of the Study:

This ***microarray*** data set provides an anal. of ***gene*** expression under brewing fermn. conditions. The data provide an insight into the various metabolic processes altered or activated by brewing conditions of growth. This study leads to future expts. whereby selective alterations in brewing conditions could be introduced to take advantage of the changing transcript profile to improve the quality of the brew.
RE.CNT 80 THERE ARE 80 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:189698 CAPLUS
DN 133:130665
TI ***Genome*** ***microarray*** analysis of transcriptional activation in multidrug resistance ***yeast*** mutants
AU DeRisi, J.; van den Hazel, B.; Marc, P.; Balzi, E.; Brown, P.; Jacq, C.; Goffeau, A.
CS Howard Hughes Medical Institute, Department of Biochemistry, Stanford University School of Medicine, Stanford, CA, USA
SO FEBS Letters (2000), 470(2), 156-160 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB The cDNA from activated mutants of the homologous transcription factors Pdr1p and Pdr3p was used to screen ***DNA*** ***microarrays*** of the ***Saccharomyces*** ***cerevisiae*** complete ***genome*** . Twenty-six overexpressed targets of the PDR1-3 and/or PDR3-7 mutants were identified. Twenty-one are new targets, the majority of which are of unknown function. In addn. to well known ABC transporters, these targets appear to be involved in transport or in membrane lipids and cell wall biosyntheses. Several of the targets seem to contribute to the cell defense against a variety of stresses. Pdr1p and Pdr3p do not act similarly on all targets. Unexpectedly, the expression of 23 other ***genes*** appeared to be repressed in the PDR1-3 and/or PDR3-7 mutants. In contrast to the majority of the activated ***genes*** , none of the repressed ***genes*** contains pleiotropic drug resistance binding sites in their promoter.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

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FILE 'CAPLUS' ENTERED AT 20:08:22 ON 17 FEB 2006
L1 5174 S ((YEAST# OR SACCHAROMYCES OR CEREVISIAE)(10A)GENOM?)/BI,AB
L2 30550 S (SEQUENCE (10A) COMPAR?)/BI,AB
L3 171023 S (ARRAY? OR MICROARRAY?)/BI,AB
L4 201026 S L2 OR L3
L5 679 S L1 AND L4
L6 672 S L5 NOT 2006/PY
L7 553 S L6 NOT 2004/PY
L8 1529420 S ((NUCLEIC(W)ACID#) OR GENE# OR DNA#)/BI,AB
L9 642 S L5 AND L8
L10 288 S (INDUSTRIAL(W)YEAST#)/BI,AB
L11 3 S L9 AND L10
L12 252207 S INDUSTRIAL/BI,AB
L13 10 S L9 AND L12
L14 397419 S ALCOHOL?/BI,AB
L15 6 S L9 AND L14
L16 5 S L15 NOT L13

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EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	4220	yeast near10 genome	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:46
L2	651	saccharomyces near10 genome	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:46
L3	789	cerevisiae near10 genome	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:46
L4	4623	l1 or l2 or l3	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:46
L5	92085	sequence near10 compar$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:46
L6	2857	l4 and l5	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:48
L7	839036	array or microarray	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:49
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L9	3474	l6 or l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:49

EAST Search History

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L13	34343	435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:50
L14	1568	702/20[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:50
L15	34721	l13 or l14	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:50
L16	847	l12 and l15	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:51
L17	376	industrial near2 yeast	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:51
L18	4	l16 and l17	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/02/17 18:51